

SEQUENCE LISTING

<110> GRIESBECK, OLIVER
HEIM, NICOLA

<120> NOVEL GENETICALLY ENCODED BIOINDICATORS OF CALCIUM-IONS

<130> 085449-0185

<140> 10/567,091
<141> 2008-07-21

<150> PCT/EP2004/008739
<151> 2004-08-04

<150> EP 03016691.2
<151> 2003-08-04

<160> 54

<170> PatentIn version 3.3

<210> 1
<211> 1863
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1	60
atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctgggt cgagctggac	60
ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgagggcga tgccacctac	120
ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc	180
ctcgtgacca ccctgacactg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag	240
cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc	300
ttcaaggacg acggcaacta caagaccgc gccgaggtga agttcgaggg cgacaccctg	360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac	420
aagctggagt acaactacat cagccacaac gtctatatca ccggccacaa gcagaagaac	480
ggcatcaagg cccacttcaa gatccgccccac aacatcgagg acggcagcgt gcagctcgcc	540
gaccactacc agcagaacac ccccatcggc gacggccccc tgctgctgcc cgacaaccac	600
tacctgagca cccagtcgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc	660
ctgctggagt tcgtgaccgc cgcccgcatg ctcagcgagg agatgattgc tgagttcaaa	720
gctgccttg acatgttga tgcggacggt ggtggggaca tcagcaccaa ggagttggc	780

acgggtgatga ggatgctggg ccagaacccc accaaagagg agctggatgc catcatcgag	840
gaggtggacg aggatggcag cggcaccatc gacttcgagg agttccctgg t gatgatggtg	900
cgccagatga aagaggacgc caagggcaag tctgaggagg agctggccaa ctgcttccgc	960
atttcgaca agaacgctga tgggttcatc gacatcgagg agctgggtga gattctcagg	1020
gccactgggg agcacgtcat cgaggaggac atagaagacc tcatgaagga ttcagacaag	1080
aacaatgacg gccgcattga cttcgatgag ttctgaaga tgatggaggg tgtgcaggag	1140
ctcatggtga gcaagggcga ggagctgttc accgggggtgg tgcccatcct ggtcgagctg	1200
gacggcgacg taaacggcca caagttcagc gtgtccggcg agggcgaggg cgatgccacc	1260
tacggcaagc tgaccctgaa gttcatctgc accaccggca agctgcccgt gccctggccc	1320
accctcgtga ccacccctcg ctacggcctg atgtgcttcg cccgctaccc cgaccacatg	1380
cgccagcacf acttcttcaa gtccgccatg cccgaaggct acgtccagga gcgcaccatc	1440
ttcttcaagg acgacggcaa ctacaagacc cgccgcgagg tgaagttcga gggcgacacc	1500
ctggtaacc gcatcgagct gaagggcatc gacttcaagg aggacggcaa catcctgggg	1560
cacaagctgg agtacaacta caacagccac aacgtctata tcatggccga caagcagaag	1620
aacggcatca aggccaaactt caagatccgc cacaacatcg aggacggcag cgtcgagctc	1680
gccgaccact accagcagaa cacccccatc ggcgacggcc ccgtgctgct gcccgacaac	1740
cactacctga gctaccagtc cccctgagc aaagacccca acgagaagcg cgatcacatg	1800
gtcctgctgg agttcgtgac cggccgggg atcactctcg gcatggacga gctgtacaag	1860
taa	1863

<210> 2
<211> 620
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Arg Met Leu Ser Glu Glu Met Ile Ala Glu Phe Lys
225 230 235 240

Ala Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr
245 250 255

Lys Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys
260 265 270

Glu Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly
275 280 285

Thr Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys
290 295 300

Glu Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg
305 310 315 320

Ile Phe Asp Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly
325 330 335

Glu Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu
340 345 350

Asp Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe
355 360 365

Asp Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Met Val Ser
370 375 380

Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu
385 390 395 400

Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu
405 410 415

Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr
420 425 430

Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr
435 440 445

Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His Asp
450 455 460

Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
465 470 475 480

Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe
485 490 495

Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe
 500 505 510

Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn
 515 520 525

Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys
 530 535 540

Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu
 545 550 555 560

Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu
 565 570 575

Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp
 580 585 590

Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala
 595 600 605

Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 610 615 620

<210> 3

<211> 1902

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 3

atggtagca agggcgagga gctgttacc ggggtggtgc ccattcttgtt cgagctggac 60

ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgagggcga tgccacctac 120

ggcaagctga ccctgaagtt catctgcacc accggcaago tgcccgtgcc ctggccccacc 180

ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccgaa ccacatgaag 240

cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatctc 300

ttcaaggacg acggcaacta caagacccgc gccgagggtga agttcgaggg cgacaccctg 360

gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420

aagctggagt acaactacat cagccacaac gtctatatca ccggccgacaa gcagaagaac 480

ggcatcaagg cccacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 540
gaccactacc agcagaacac ccccatcgcc gacggccccg tgctgctgcc cgacaaccac 600
tacctgagca cccagtcgc cctgagcaaa gacccaacg agaagcgcga tcacatggtc 660
ctgctggagt tcgtgaccgc cgccccatg ctaatggatg acatctacaa ggctgcggta 720
gagcagctga cagaagagca gaaaaatgag ttcaaggcag cttcgacat cttcgtgctg 780
ggcgctgagg atggctgcat cagcaccaag gagctggca aggtgatgag gatgctggc 840
cagaacccca cccctgagga gctgcaggag atgatcgatg aggtggacga ggacggcagc 900
ggcacggtgg actttgatga gttcctggtc atgatggttc ggtgcattgaa ggacgacagc 960
aaaggaaaat ctgaggagga gctgtctgac ctcttccgca tggatgacaa aaatgctgat 1020
ggctacatcg acctggatga gctgaagata atgctgcagg ctacaggcga gaccatcacf 1080
gaggacgaca tcgaggaact catgaaggac ggagacaaga acaacgacgg ccgcacatcgac 1140
tatgatgagt tcctggagtt catgaagggt gtggaggagc tcatggtgag caagggcgag 1200
gagctgttca ccgggggttgtt gcccattctg gtcgagctgg acggcgacgt aaacggccac 1260
aagttcagcg tgtccggcga gggcgagggc gatgccacct acggcaagct gaccctgaag 1320
ttcatctgca ccaccggcaa gctgcccgtg ccctggccca ccctcgtgac caccttcggc 1380
tacggcctga tgtgcttcgc ccgctacccc gaccacatgc gccagcacga cttcttcaag 1440
tccgccatgc ccgaaggcta cgtccaggag cgacccatct tcttcaagga cgacggcaac 1500
tacaagaccc gcggcgaggt gaagttcgag ggcgacaccc tggtaaccg catcgagctg 1560
aagggcatcg acttcaagga ggacggcaac atcctggggc acaagctgga gtacaactac 1620
aacagccaca acgtctatat catggccgac aagcagaaga acggcatcaa ggccaaacttc 1680
aagatccgcc acaacatcgaa ggacggcagc gtgcagctcg ccgaccacta ccagcagaac 1740
accccatcg gcgacggccc cgtgctgctg cccgacaaacc actacctgag ctaccagtcc 1800
gccctgagca aagaccccaa cgagaagcgc gatcacaatgg tcctgctgga gttcgtgacc 1860
ggcgccggaa tcactctcgg catggacgag ctgtacaatg aa 1902

<210> 4
<211> 633
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 4
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Arg Met Leu Met Asp Asp Ile Tyr Lys Ala Ala Val
 225 230 235 240

Glu Gln Leu Thr Glu Glu Gln Lys Asn Glu Phe Lys Ala Ala Phe Asp
 245 250 255

Ile Phe Val Leu Gly Ala Glu Asp Gly Cys Ile Ser Thr Lys Glu Leu
 260 265 270

Gly Lys Val Met Arg Met Leu Gly Gln Asn Pro Thr Pro Glu Glu Leu
 275 280 285

Gln Glu Met Ile Asp Glu Val Asp Glu Asp Gly Ser Gly Thr Val Asp
 290 295 300

Phe Asp Glu Phe Leu Val Met Met Val Arg Cys Met Lys Asp Asp Ser
 305 310 315 320

Lys Gly Lys Ser Glu Glu Leu Ser Asp Leu Phe Arg Met Phe Asp
 325 330 335

Lys Asn Ala Asp Gly Tyr Ile Asp Leu Asp Glu Leu Lys Ile Met Leu
 340 345 350

Gln Ala Thr Gly Glu Thr Ile Thr Glu Asp Asp Ile Glu Glu Leu Met
 355 360 365

Lys Asp Gly Asp Lys Asn Asn Asp Gly Arg Ile Asp Tyr Asp Glu Phe
 370 375 380

Leu Glu Phe Met Lys Gly Val Glu Glu Leu Met Val Ser Lys Gly Glu
 385 390 395 400

Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp
 405 410 415

Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala
 420 425 430

Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu
 435 440 445

Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met
 450 455 460

Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His Asp Phe Phe Lys
 465 470 475 480

Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys
 485 490 495

Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
 500 505 510

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
 515 520 525

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
 530 535 540

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
 545 550 555 560

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
 565 570 575

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
 580 585 590

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
 595 600 605

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
 610 615 620

Thr Leu Gly Met Asp Glu Leu Tyr Lys
 625 630

<210> 5

<211> 1863

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 5

atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac 60

ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgagggcga tgccacctac	120
ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggccccacc	180
ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccgaa ccacatgaag	240
cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatctc	300
ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg	360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac	420
aagctggagt acaactacat cagccacaac gtctatatca ccgcccacaa gcagaagaac	480
ggcatcaagg cccacttcaa gatccgcccc acatcgagg acggcagcgt gcagctcgcc	540
gaccactacc agcagaacac ccccatcgcc gacggccccc tgctgctgcc cgacaaccac	600
tacctgagca cccagtcgc cctgagcaaa gaccccaacg agaagcgcga tcacatggc	660
ctgctggagt tcgtgaccgc cgcccgcatg ctcagcgagg agatgattgc tgagttcaaa	720
gctgccttg acatgttga tgccggacggt ggtggggaca tcagcaccaa ggagttggc	780
acggtgatga ggatgctggg ccagaacccc accaaagagg agctggatgc catcatcgag	840
gaggtggacg aggatggcag cggcaccatc gacttcgagg agttcctggg gatgatggg	900
cggccagatga aagaggacgc caagggcaag tctgaggagg agctggccaa ctgcttccgc	960
atcttcgcca agaacgctga tgggttcatc gacatcgagg agctgggtga gattctcagg	1020
gccactgggg agcacgtcat cgaggaggac atagaagacc tcatgaagga ttcagacaag	1080
aacaatgacg gccgcattga cttcgatgag ttctgaaga tggatggggg tgtgcaggag	1140
ctcatggtga gcaagggcga ggagctttc accgggggtgg tgcccatcct ggtcgagctg	1200
gacggcgacg taaacggcca caagttcagc gtgtccggcg agggcgaggg cgatgccacc	1260
tacggcaagc tgaccctgaa gttcatctgc accacccggca agctgcccgt gcccggccc	1320
accctcgtga ccacccctcg ctacggcctg atgtgcttcg cccgctaccc cgaccacatg	1380
cggccagcacg acttcttcaa gtccgccatg cccgaaggct acgtccagga ggcgaccatc	1440
ttcttcagg acgacggcaa ctacaagacc cgcgcggagg tgaagttcga gggcgacacc	1500
ctgggtgaacc gcatcgagct gaagggcatc gacttcaagg aggacggcaa catcctgggg	1560
cacaagctgg agtacaacta caacagccac aacgtctata tcatggccga caagcagaag	1620
aacggcatca aggccaaactt caagatccgc cacaacatcg aggacggcag cgtcgagctc	1680
gccgaccact accagcagaa caccccccattc ggcgacggcc ccgtgctgct gcccgacaac	1740
cactacctga gctaccagtc cggccctgagc aaagacccca acgagaagcg cgatcacatg	1800

gtcctgctgg agttcggtac cgccgcggg atcaactctcg gcatggacga gctgtacaag 1860
 taa 1863

<210> 6
 <211> 620
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 6
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Arg Met Leu Ser Glu Glu Met Ile Ala Glu Phe Lys
225 230 235 240

Ala Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Asp Ile Ser Thr
245 250 255

Lys Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys
260 265 270

Glu Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly
275 280 285

Thr Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys
290 295 300

Glu Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg
305 310 315 320

Ile Phe Ala Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly
325 330 335

Glu Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu
340 345 350

Asp Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe
355 360 365

Asp Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Met Val Ser
370 375 380

Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu
385 390 395 400

Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu
405 410 415

Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr
420 425 430

Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr
435 440 445

Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His Asp
450 455 460

Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
465 470 475 480

Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe
485 490 495

Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe
500 505 510

Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn
515 520 525

Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys
530 535 540

Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu
545 550 555 560

Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu
565 570 575

Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp
580 585 590

Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala
595 600 605

Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
610 615 620

<210> 7
<211> 1908
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 7						
atggtgagca	agggcgagga	gctgttcacc	ggggtgtgtgc	ccatcctgggt	cgagctggac	60
ggcgacgtaa	acggccacag	gttcagcgtg	tccggcgagg	gcgaggggcga	tgccacctac	120
ggcaagctga	ccctgaagtt	catctgcacc	accggcaagc	tgcccgtgcc	ctggcccacc	180
ctcgtgacca	ccctgacctg	gggcgtgcag	tgcttcagcc	gctaccccgaa	ccacatgaag	240
cagcacgact	tcttcaagtc	cgccatgccc	gaaggctacg	tccaggagcg	taccatttc	300
ttcaaggacg	acggcaacta	caagaccgc	gccgaggtga	agttcgaggg	cgacaccctg	360
gtgaaccgca	tcgagctgaa	gggcattcgac	ttcaaggagg	acggcaacat	cctggggcac	420
aagctggagt	acaactacat	cagccacaac	gtctatatca	ccgcccacaa	gcagaagaac	480
ggcatcaagg	cccacttcaa	gatccgcccc	aacatcgagg	acggcagcgt	gcagctcgcc	540
gaccactacc	agcagaacac	ccccatcgcc	gacggccccc	tgctgctgcc	cgacaaccac	600
tacctgagca	cccagtccgc	cctgagcaaa	gaccccaacg	agaagcgcga	tcacatggtc	660
ctgctggagt	tcgtgaccgc	cgcccgcatg	ctaattggcgt	caatgacgga	ccagcaggcg	720
gaggcccgcg	ccttcctcag	cgaggagatg	attgctgagt	tcaaagctgc	ctttgacatg	780
ttttagatgcgg	acggtggtgg	ggacatcagc	accaaggagt	tgggcacgg	gatgaggatg	840
ctggggccaga	accccaccaa	agaggagctg	gatccatca	tcgaggaggt	ggacgaggat	900
ggcagcggca	ccatcgactt	cgaggagttc	ctgggtgatga	tggtgccca	gatgaaagag	960
gacgccaagg	gcaagtctga	ggaggagctg	gccaactgct	tccgcattt	cgacaagaac	1020
gctgatgggt	tcatcgacat	cgaggagctg	ggtgagattc	tcagggccac	tggggagcac	1080
gtcatacgagg	aggacataga	agacatcgatg	aaggattcag	acaagaacaa	tgacggccgc	1140
attgacttcg	atgagttcct	gaagatgatg	gagggtgtgc	aggagctcat	ggtgagcaag	1200
ggcgaggagc	tgttcaccgg	ggtgggtgcc	atcctggcgt	agctggacgg	cgacgtaaac	1260
ggccacaagt	tcagcgtgtc	cgccgagggc	gagggcgatg	ccacctacgg	caagctgacc	1320
ctgaagttca	tctgcaccac	cgcaagctg	cccgtgccct	ggcccaccct	cgtgaccacc	1380
ttcggctacg	gcctgatgtg	cttcgcccc	taccccgacc	acatgogcca	gcacgacttc	1440

ttcaagtccg ccatgcccgaa aggctacgtc caggagcgca ccatcttctt caaggacgac	1500
ggcaactaca agaccgcgc cgaggtgaag ttcgagggcg acaccctgggt gaaccgcac	1560
gagctgaagg gcatcgactt caaggaggac ggcaacatcc tggggcacaa gctggagtac	1620
aactacaaca gccacaacgt ctatcatg gcccacaaggcagaagaacacgg catcaaggcc	1680
aacttcaaga tccgcccccaa catcgaggac ggcagcgtgc agctcgccga ccactaccag	1740
cagaacaccc ccatcgccgaa cggcccccgtg ctgctgcccga acaaccacta cctgagctac	1800
cagtcgcgccc tgagcaaaga ccccaacgag aagcgcgatc acatggcct gctggagttc	1860
gtgaccgccc cggggatcac tctcggcatg gacgagctgt acaagtaa	1908

<210> 8

<211> 635

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 8

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly		
20	25	30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
35	40	45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
50	55	60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys			
65	70	75	80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
85	90	95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
100	105	110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
115	120	125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Arg Met Leu Met Ala Ser Met Thr Asp Gln Gln Ala
225 230 235 240

Glu Ala Arg Ala Phe Leu Ser Glu Glu Met Ile Ala Glu Phe Lys Ala
245 250 255

Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Asp Ile Ser Thr Lys
260 265 270

Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys Glu
275 280 285

Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr
290 295 300

Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu
305 310 315 320

Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg Ile
325 330 335

Phe Asp Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly Glu
340 345 350

Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu Asp
 355 360 365

Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe Asp
 370 375 380

Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Met Val Ser Lys
 385 390 395 400

Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
 405 410 415

Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
 420 425 430

Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
 435 440 445

Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly
 450 455 460

Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His Asp Phe
 465 470 475 480

Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
 485 490 495

Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
 500 505 510

Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
 515 520 525

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
 530 535 540

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
 545 550 555 560

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
 565 570 575

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 580 585 590

Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
595 600 605

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
610 615 620

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
625 630 635

```
<210> 9  
<211> 1542  
<212> DNA  
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 9
atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac 60
ggcgaactaa acggccacag gttcagcgtg tccggcgagg gcgagggcga tgccacctac 120
ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 180
ctcgtgacca ccctgacctg gggcgtgcag tgttcagcc gctaccccgaa ccacatgaag 240
cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc 300
ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg 360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420
aagctggagt acaactacat cagccacaac gtctatatca cccggcacaac gcagaagaac 480
ggcatcaagg cccacttcaa gatccgcccac aacatcgagg acggcagcgt gcagctcgcc 540
gaccactacc agcagaacac ccccatcgac gacggccccg tgctgctgcc cgacaaccac 600
tacctgagca cccagtccgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc 660
ctgctggagt tcgtgaccgc cgcccgcatg cttaggccaga accccaccaa agaggagctg 720
gatgccatca tcgaggaggt ggacgaggat ggcagcggca ccatcgactt cgaggagttc 780
ctgggtatga tggtgccca gatgaaagag gacgcccggc tcattggtag caagggcgag 840
gagctgtca ccgggggtggt gcccattctg gtcgagctgg acggcgcacgt aaacggccac 900
aagttcagcg tgtccggcga gggcgagggc gatgccacct acggcaagct gaccctgaaag 960
ttcatctgca ccacccggcaa gctgccccgtg ccctggccca ccctcggtac caccttcggc 1020

tacggcctga	tgtgcttcgc	ccgctacccc	gaccacatgc	gccagcacga	cttcttcaag	1080
tccgccccatgc	ccgaaggcta	cgtccaggag	cgcaccatct	tcttcaagga	cgacggcaac	1140
tacaagaccc	gcccggaggt	gaagttcgag	ggcgacacccc	tggtaaccg	catcgagctg	1200
aagggcatcg	acttcaagga	ggacggcaac	atcctggggc	acaagctgga	gtacaactac	1260
aacagccaca	acgtctatat	catggccgac	aagcagaaga	acggcatcaa	ggccaacttc	1320
aagatccgcc	acaacatcga	ggacggcagc	gtcagctcg	ccgaccacta	ccagcagaac	1380
accccccattcg	gcgacggccc	cgtgctgctg	cccgacaacc	actacctgag	ctaccagtcc	1440
gccctgagca	aagacccaa	cgagaagcgc	gatcacatgg	tcctgctgga	gttcgtgacc	1500
gccgccccggga	tcactctcg	catggacgag	ctgtacaagt	aa		1542

<210> 10

<211> 513

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 10

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1					5				10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Arg	Phe	Ser	Val	Ser	Gly
						20			25				30		

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
						35			40				45		

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
						50			55			60			

Leu	Thr	Trp	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
					65			70			75		80		

Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
							85			90			95		

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
						100			105				110		

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Arg Met Leu Gly Gln Asn Pro Thr Lys Glu Glu Leu
 225 230 235 240

Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp
 245 250 255

Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu Asp Ala
 260 265 270

Glu Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
 275 280 285

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
 290 295 300

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
 305 310 315 320

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
 325 330 335

Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His
 340 345 350

Met Arg Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
355 360 365

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
370 375 380

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
385 390 395 400

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
405 410 . 415

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 420 425 430

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 435 440 445

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
450 455 460

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
465 470 475 480

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
485 490 495

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 500 505 510

Lys

```
<210> 11
<211> 2469
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 11
atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggc cgagctggac 60

ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgagggcga tgccacctac	120
ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc	180
ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag	240
cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc	300
ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg	360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac	420
aagctggagt acaactacat cagccacaac gtctatatca ccgcccacaa gcagaagaac	480
ggcatcaagg cccacttcaa gatccgcccc acatcgagg acggcagcgt gcagctcgcc	540
gaccactaacc agcagaacac ccccatcgcc gacggccccc tgctgctgcc cgacaaccac	600
tacctgagca cccagteccgc cctgagcaaaa gaccccaacg agaagcgcga tcacatggtc	660
ctgctggagt tcgtgaccgc cgcccgcatg ctaatggcgt caatgacgga ccagcaggcg	720
gaggcccgcg cttcctcag cgaggagatg attgctgagt tcaaagctgc ctttgacatg	780
ttttagatgcgg acgggtgggg ggacatcagc accaaggagt tgggcacgggt gatgaggatg	840
ctggggccaga accccaccaa agaggagctg gatgccatca tcgaggaggt ggacgaggat	900
ggcagcggca ccatcgactt cgaggagttc ctggtgatga tggtgcccca gatgaaagag	960
gacgccaagg gcaagtctga ggaggagctg gccaactgct tccgcattt cgacaagaac	1020
gctgatgggt tcatcgacat cgaggagctg ggtgagattc tcagggccac tggggagcac	1080
gtcatcgagg aggacataga agacctcatg aaggattcag acaagaacaa tgacggccgc	1140
attgacttcg atgagttcct gaagatgatg gagggtgtgc aggagctcgg cggcatgtct	1200
gatgaagaga aaaagcgtcg tgcagccacc gcccgtcgtc agcacctgaa gagtgctatg	1260
ctccagcttg ctgtcactga aatagaaaaa gaagcagctg ctaaagaagt ggaaaagcaa	1320
aactacctgg cagagcatag ccctcctctg tccctccag ggtccatgca ggaacttcag	1380
gaactgagca aaaaacttca tgccaagata gactcagtgg atgagggaaag gtatgacaca	1440
gaggtgaagc tacagaagac taacaaggag ctggaggacc tgagccagaa gctgtttgac	1500
ctgagggggca agttcaagag gccacctctg cgccgggtgc gcatgtctgc tcatgccatg	1560
ctgcgtgccc tgctgggctc caagcacaag gtcaacatgg acctccgggc caacctgaag	1620
caagtcaaga aggaggacac ggagaaggag aaggacctcc gcgatgtggg tgactggagg	1680
aagaacattg aggagaaatc tggcatggag ggcaggaaga agatgttga ggccggcgag	1740
tccgagctca tggtgagcaa gggcgaggag ctgttcaccg gggtggtgcc catcctggtc	1800

gagctggacg	gcgacgtaaa	cggccacaag	ttcagcgtgt	ccggcgaggg	cgagggcgat	1860
gccacctacg	gcaagctgac	cctgaagtgc	atctgcacca	ccggcaagct	gcccggtgccc	1920
tggcccaccc	tcgtgaccac	cttcggctac	ggcctgatgt	gcttcgcccc	ctaccccgac	1980
cacatgcgcc	agcacgactt	cttcaagtcc	gccatgcccc	aaggctacgt	ccaggagcgc	2040
accatcttct	tcaaggacga	cggcaactac	aagacccgcg	ccgaggtgaa	gttcgagggc	2100
gacaccctgg	tgaaccgcat	cgagctgaag	ggcatcgact	tcaaggagga	cgccaacatc	2160
ctggggcaca	agctggagta	caactacaac	agccacaacg	tctatatcat	ggccgacaag	2220
cagaagaacg	gcatcaaggc	caacttcaag	atccgccaca	acatcgagga	cggcagcgtg	2280
cagctcgccg	accactacca	gcagaacacc	cccatcggcg	acggccccgt	gctgctgccc	2340
gacaaccact	acctgagcta	ccagtccgcc	ctgagcaaag	accccaacga	gaagcgcgat	2400
cacatggtcc	tgctggagtt	cgtgaccgcc	gccgggatca	ctctcggcat	ggacgagctg	2460
tacaagtaa						2469

<210> 12

<211> 822

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 12

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Arg	Phe	Ser	Val	Ser	Gly
			20				25					30			

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
				35			40				45				

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
				50			55			60					

Leu	Thr	Trp	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
				65			70			75				80	

Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
					85				90				95		

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Arg Met Leu Met Ala Ser Met Thr Asp Gln Gln Ala
 225 230 235 240

Glu Ala Arg Ala Phe Leu Ser Glu Glu Met Ile Ala Glu Phe Lys Ala
 245 250 255

Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Asp Ile Ser Thr Lys
 260 265 270

Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys Glu
 275 280 285

Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr
 290 295 300

Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu
 305 310 315 320

Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg Ile
 325 330 335

Phe Asp Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly Glu
 340 345 350

Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu Asp
 355 360 365

Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe Asp
 370 375 380

Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Gly Gly Met Ser
 385 390 395 400

Asp Glu Glu Lys Lys Arg Arg Ala Ala Thr Ala Arg Arg Gln His Leu
 405 410 415

Lys Ser Ala Met Leu Gln Leu Ala Val Thr Glu Ile Glu Lys Glu Ala
 420 425 430

Ala Ala Lys Glu Val Glu Lys Gln Asn Tyr Leu Ala Glu His Ser Pro
 435 440 445

Pro Leu Ser Leu Pro Gly Ser Met Gln Glu Leu Gln Glu Leu Ser Lys
 450 455 460

Lys Leu His Ala Lys Ile Asp Ser Val Asp Glu Glu Arg Tyr Asp Thr
 465 470 475 480

Glu Val Lys Leu Gln Lys Thr Asn Lys Glu Leu Glu Asp Leu Ser Gln
 485 490 495

Lys Leu Phe Asp Leu Arg Gly Lys Phe Lys Arg Pro Pro Leu Arg Arg
 500 505 510

Val Arg Met Ser Ala Asp Ala Met Leu Arg Ala Leu Leu Gly Ser Lys
 515 520 525

His Lys Val Asn Met Asp Leu Arg Ala Asn Leu Lys Gln Val Lys Lys
 530 535 540

Glu Asp Thr Glu Lys Glu Lys Asp Leu Arg Asp Val Gly Asp Trp Arg
 545 550 555 560

Lys Asn Ile Glu Glu Lys Ser Gly Met Glu Gly Arg Lys Lys Met Phe
 565 570 575

Glu Ala Gly Glu Ser Glu Leu Met Val Ser Lys Gly Glu Glu Leu Phe
 580 585 590

Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly
 595 600 605

His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly
 610 615 620

Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
 625 630 635 640

Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe Ala
 645 650 655

Arg Tyr Pro Asp His Met Arg Gln His Asp Phe Phe Lys Ser Ala Met
 660 665 670

Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly
 675 680 685

Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val
 690 695 700

Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile
 705 710 715 720

Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile
 725 730 735

Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg
 740 745 750

His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln
 755 760 765

Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr
 770 775 780

Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp
 785 790 795 800

His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly
 805 810 815

Met Asp Glu Leu Tyr Lys
 820

<210> 13
 <211> 1959
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 13		
atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatacctgggt cgagactggac	60	
ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgaggggcga tgccacacctac	120	
ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggccccacc	180	
ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccgaa ccacatgaag	240	
cagcacgact tcttcaagtc cgcattgtccc gaaggctacg tccaggagcg taccatcttc	300	
ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg	360	
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac	420	
aagctggagt acaactacat cagccacaac gtcttatatca ccggccgacaa gcagaagaac	480	
ggcatcaagg cccacttcaa gatccgcccc aacatcgagg acggcaagcgt gcagctcgcc	540	
gaccactacc agcagaacac ccccatcgcc gacggccccg tgctgctgcc cgacaaccac	600	
tacctgagca cccagtccgc cctgagcaaa gacccaacg agaagcgcga tcacatggtc	660	
ctgctggagt tcgtgaccgc cgcccgcatg ctcgctgatg ccatgctgcg tgccctgctg	720	
ggctccaagc acaaggtcaa cggcgccgcg tcaatgacgg accagcaggc ggaggcccc	780	
gccttcctca gcgaggagat gattgctgag ttcaaagctg cctttgacat gtttgatgctg	840	
gacgggtggtg gggacatcag caccaaggag ttgggcacgg tggatgaggat gctggccag	900	
aaccccacca aagaggagct ggatgccatc atcgaggagg tggacgagga tggcagcggc	960	
accatcgact tcgaggagtt cctgggtatg atggtgcgcc agatgaaaga ggacgccaag	1020	
ggcaagtctg aggaggagct ggccaaactgc ttccgcataat tcgacaagaa cgctgatggg	1080	

ttcatcgaca tcgaggagct gggtagatt ctcagggcca ctggggagca cgtcatcgag	1140
gaggacata g aagacctcat gaaggattca gacaagaaca atgacggccg cattgactc	1200
gatgagttcc tgaagatgtat ggagggtgtg caggagctca tggtgagcaa gggcgaggag	1260
ctgttacccg gggtggtgcc catcctggtc gagctggacg gcgacgtaaa cggccacaag	1320
ttcagcgtgt ccggcgaggg cgagggcgat gccacctacg gcaagctgac cctgaagtcc	1380
atctgcacca cggcaagct gcccgtgccc tggcccaccc tcgtgaccac cttcggtac	1440
ggcctgatgt gttcgccccg ctaccccgac cacatgcgcc agcacgactt cttcaagtcc	1500
gcatgccccg aaggctacgt ccaggagcgc accatcttct tcaaggacga cggcaactac	1560
aagacccgcg ccgaggtgaa gttcgagggc gacaccctgg tgaaccgcat cgagctgaag	1620
ggcatcgact tcaaggagga cggcaacatc ctggggcaca agctggagta caactacaac	1680
agccacaacg tctatatcat ggccgacaag cagaagaacg gcatcaaggc caacttcaag	1740
atccgcccaca acatcgagga cggcagcgtg cagctcgccg accactacca gcagaacacc	1800
cccatcgccg acggccccgt gctgctgccc gacaaccact acctgagcta ccagtccgcc	1860
ctgagcaaag accccaacga gaagcgcat cacatggtcc tgctggagtt cgtgaccgcc	1920
gccgggatca ctctcgcat ggacgagctg tacaagtaa	1959

<210> 14

<211> 652

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 14

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly			
20	25	30	

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35	40	45	

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50	55	60	

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Arg Met Leu Ala Asp Ala Met Leu Arg Ala Leu Leu
225 230 235 240

Gly Ser Lys His Lys Val Asn Gly Gly Ala Ser Met Thr Asp Gln Gln
245 250 255

Ala Glu Ala Arg Ala Phe Leu Ser Glu Glu Met Ile Ala Glu Phe Lys
260 265 270

Ala Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr
275 280 285

Lys Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys
290 295 300

Glu Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly
 305 310 315 320

Thr Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys
 325 330 335

Glu Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg
 340 345 350

Ile Phe Asp Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly
 355 360 365

Glu Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu
 370 375 380

Asp Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe
 385 390 395 400

Asp Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Met Val Ser
 405 410 415

Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu
 420 425 430

Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu
 435 440 445

Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr
 450 455 460

Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr
 465 470 475 480

Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His Asp
 485 490 495

Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
 500 505 510

Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe
 515 520 525

Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe
 530 535 540

Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn
545 550 555 560

Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys
 565 570 575

Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu
580 585 590

Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu
 595 600 605

Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp
610 615 620

Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala
625 630 635 640

Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
645 650

```
<210> 15
<211> 1827
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 15
atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac 60
ggcgacgtaa acggcccacag gttcagcgtg tccggcgagg gcgagggcga tgccacctac 120
ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 180
ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccgaa ccacatgaag 240
cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc 300
ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg 360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420
aaqctqqaqt acaaactacat cagccacaac gtctatatca ccggccgacaa gcagaagaac 480

ggcatcaagg cccacttcaa gatccgcccc aacatcgagg acggcagcgt gcagctcgcc	540
gaccactacc agcagaacac ccccattcgcc gacggccccg tgctgctgcc cgacaaccac	600
tacctgagca cccagtcgc cctgagcaaa gaccccaacg agaagcgcga tcacatggc	660
ctgctggagt tcgtgaccgc cggccgcattg cttagacctga gccagaagct gtttgacctg	720
aggggcaagt tcaagaggcc acctctgcgc cgggtgcgc tgtctgctga tgccatgctg	780
cgtgcctgc tgggtccaa gcacaaggc ggcagcggca gcatgctaatt ggcgtcaatg	840
acggaccagc aggccggaggc ccgcgccttc cttagcgagg agatgattgc tgagttcaaa	900
gctgccttg acatgttga tgcggacggt ggtggggaca tcagcaccaa ggagttggc	960
acgggtatga ggatgctggg ccagaacccc accaaagagg agctggatgc catcatcgag	1020
gaggtggacg aggtggcag cggcaccatc gacttcgagg agttccttgt gatgatggc	1080
cggccagatga aagaggacgc cgagctcatg gtgagcaagg gcgaggagct gttcacccgg	1140
gtgggtccca tcctggtcga gctggacggc gacgtaaacg gccacaagtt cagcgtgtcc	1200
ggcgagggcg agggcgatgc cacctacggc aagctgaccc tgaagttcat ctgcaccacc	1260
ggcaagctgc ccgtgcctg gcccaccctc gtgaccaccc tggctacgg cctgatgtgc	1320
ttcgcccgct accccgacca catgcgcacg cacgacttct tcaagtccgc catgcccga	1380
ggctacgtcc aggagcgcac catcttcttc aaggacgacg gcaactacaa gaccgcgc	1440
gaggtgaagt tcgagggcga caccctggtg aaccgcacg agctgaaggg catcgacttc	1500
aaggaggacg gcaacatcct ggggcacaag ctggagtaca actacaacag ccacaacgtc	1560
tatatcatgg ccgacaagca gaagaacggc atcaaggcca acttcaagat ccgcccacaac	1620
atcgaggacg gcagcgtgca gctcgccgac cactaccacg agaacacccc catcgccgac	1680
ggccccgtgc tgctgcccga caaccactac ctgagctacc agtccgcct gagcaaagac	1740
cccaacgaga agcgcgatca catggccttg ctggagttcg tgaccgcgc cgggatcact	1800
ctcggcatgg acgagctgta caagtaa	1827

<210> 16
 <211> 608
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 16

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Arg	Phe	Ser	Val	Ser	Gly
	20					25						30			

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
	35				40				45						

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50				55				60						

Leu	Thr	Trp	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
	65			70				75					80		

Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
	85				90							95			

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
	100				105							110			

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
	115					120						125			

Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
	130				135				140						

Asn	Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn
	145					150			155				160		

Gly	Ile	Lys	Ala	His	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
	165						170					175			

Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
	180					185						190			

Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
	195				200							205			

Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
	210				215						220				

Val Thr Ala Ala Arg Met Leu Asp Leu Ser Gln Lys Leu Phe Asp Leu
 225 230 235 240

Arg Gly Lys Phe Lys Arg Pro Pro Leu Arg Arg Val Arg Met Ser Ala
 245 250 255

Asp Ala Met Leu Arg Ala Leu Leu Gly Ser Lys His Lys Val Gly Ser
 260 265 270

Gly Ser Met Leu Met Ala Ser Met Thr Asp Gln Gln Ala Glu Ala Arg
 275 280 285

Ala Phe Leu Ser Glu Glu Met Ile Ala Glu Phe Lys Ala Ala Phe Asp
 290 295 300

Met Phe Asp Ala Asp Gly Gly Asp Ile Ser Thr Lys Glu Leu Gly
 305 310 315 320

Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys Glu Glu Leu Asp
 325 330 335

Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp Phe
 340 345 350

Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu Asp Ala Glu
 355 360 365

Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 370 375 380

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
 385 390 395 400

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 405 410 415

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 420 425 430

Thr Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met
 435 440 445

Arg Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 450 455 460

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 465 470 475 480

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 485 490 495

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 500 505 510

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 515 520 525

Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 530 535 540

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 545 550 555 560

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
 565 570 575

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 580 585 590

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 595 600 605

<210> 17

<211> 1869

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 17

atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctgggt cgagctggac 60

ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgaggcgta tgccacctac 120

ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 180

ctcgtgacca ccctgacactg gggcggtgcag tgcttcagcc gctaccccgaa ccacatgaag 240

cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc 300

ttcaaggacg acggcaacta caagaccgc gccgaggtga agttcgaggg cgacaccctg	360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac	420
aagctggagt acaactacat cagccacaac gtctatatca ccgcccacaa gcagaagaac	480
ggcatcaagg cccacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc	540
gaccactacc agcagaacac ccccattcgc gacggccccc tgctgctgcc cgacaaccac	600
tacctgagca cccagtcgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc	660
ctgctggagt tcgtgaccgc cgcccgcatg ctgctgacag aagagcagaa aaatgagttc	720
aaggcagcct tcgacatctt cgtgctggc gctgaggatg gctgcatcag caccaggag	780
ctgggcaagg ttagtggat gctggccag aaccccaccc ctgaggagct gcaggagatg	840
atcgatgagg tggacgagga cggcagcgc acggtgact ttgatgagtt cttggtcatg	900
atggttcggt gcatgaagga cgacagcaaa gggaaatctg aggaggagct gtctgacctc	960
ttccgcatgt ttgacaaaaa tgctgatggc tacatcgacc tggatgagct gaagataatg	1020
ctgcaggcta caggcgagac catcacggag gacgacatcg aggaactcat gaaggacgga	1080
gacaagaaca acgacggccg catcgactat gatgagttcc tggagttcat gaagggtgt	1140
gaggagctca tggtagcaaa gggcgaggag ctgttcaccg gggtaggtgcc catcctggtc	1200
gagctggacg gcgacgtaaa cggccacaag ttcaagctgt ccggcgaggg cgagggcgt	1260
gccacctacg gcaagctgac cctgaagttc atctgcacca ccggcaagct gcccgtgcc	1320
tggcccaccc tcgtgaccac cttcggtac ggctgatgt gcttcgccc ctaccccgac	1380
cacatgcgcc agcacgactt cttcaagtcc gccatgccc aaggctacgt ccaggagcgc	1440
accatcttct tcaaggacga cggcaactac aagacccgcg ccgaggtgaa gttcgagggc	1500
gacaccctgg tgaaccgcat cgagctgaag ggcacatcgact tcaaggagga cggcaacatc	1560
ctggggcaca agctggagta caactacaac agccacaacg tctatatcat ggccgacaag	1620
cagaagaacg gcatcaaggc caacttcaag atccgcccaca acatcgagga cggcagcgt	1680
cagctcgccg accactacca gcagaacacc cccatcgccg acggcccccgt gctgctgcc	1740
gacaaccact acctgagcta ccagtccgcc ctgagcaag accccaacga gaagcgcgt	1800
cacatggtcc tgctggagtt cgtgaccgcc gccggatca ctctcggcat ggacgagctg	1860
tacaagtaa	1869

<210> 18
<211> 622
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 18
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Arg Met Leu Leu Thr Glu Glu Gln Lys Asn Glu Phe
 225 230 235 240

Lys Ala Ala Phe Asp Ile Phe Val Leu Gly Ala Glu Asp Gly Cys Ile
 245 250 255

Ser Thr Lys Glu Leu Gly Lys Val Met Arg Met Leu Gly Gln Asn Pro
 260 265 270

Thr Pro Glu Glu Leu Gln Glu Met Ile Asp Glu Val Asp Glu Asp Gly
 275 280 285

Ser Gly Thr Val Asp Phe Asp Glu Phe Leu Val Met Met Val Arg Cys
 290 295 300

Met Lys Asp Asp Ser Lys Gly Lys Ser Glu Glu Glu Leu Ser Asp Leu
 305 310 315 320

Phe Arg Met Phe Asp Lys Asn Ala Asp Gly Tyr Ile Asp Leu Asp Glu
 325 330 335

Leu Lys Ile Met Leu Gln Ala Thr Gly Glu Thr Ile Thr Glu Asp Asp
 340 345 350

Ile Glu Glu Leu Met Lys Asp Gly Asp Lys Asn Asn Asp Gly Arg Ile
 355 360 365

Asp Tyr Asp Glu Phe Leu Glu Phe Met Lys Gly Val Glu Glu Leu Met
 370 375 380

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 385 390 395 400

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 405 410 415

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 420 425 430

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 435 440 445

Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln
 450 455 460

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 465 470 475 480

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 485 490 495

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 500 505 510

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 515 520 525

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 530 535 540

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 545 550 555 560

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 565 570 575

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser
 580 585 590

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 595 600 605

Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 610 615 620

<210> 19

<211> 486

<212> DNA

<213> Homo sapiens

<400> 19

atggatgaca tctacaaggc tgccgttagag cagctgacag aagagcagaa aatgagtgc 60

aaggcagcct tcgacatctt cgtgctggc gctgaggatg gctgcatacg caccaaggag	120
ctggcaagg ttaggaggat gctggccag aaccccaccc ctgaggagct gcaggagatg	180
atcgatgagg tggacgagga cggcagccgc acggtgact ttgatgagtt cctggtcatg	240
atggttcggt gcatgaagga cgacagcaaa gggaaatctg aggaggagct gtctgacc	300
ttccgcattgt ttgacaaaaa tgctgatggc tacatcgacc tggatgagct gaagataatg	360
ctgcaggcta caggcgagac catcacggag gacgacatcg aggagctcat gaaggacgga	420
gacaagaaca acgacggccg catcgactat gatgagttcc tggagttcat gaagggtgtg	480
gagtag	486

<210> 20

<211> 161

<212> PRT

<213> Homo sapiens

<400> 20

Met Asp Asp Ile Tyr Lys Ala Ala Val Glu Gln Leu Thr Glu Glu Gln			
1	5	10	15

Lys Asn Glu Phe Lys Ala Ala Phe Asp Ile Phe Val Leu Gly Ala Glu		
20	25	30

Asp Gly Cys Ile Ser Thr Lys Glu Leu Gly Lys Val Met Arg Met Leu		
35	40	45

Gly Gln Asn Pro Thr Pro Glu Glu Leu Gln Glu Met Ile Asp Glu Val		
50	55	60

Asp Glu Asp Gly Ser Gly Thr Val Asp Phe Asp Glu Phe Leu Val Met			
65	70	75	80

Met Val Arg Cys Met Lys Asp Asp Ser Lys Gly Lys Ser Glu Glu Glu		
85	90	95

Leu Ser Asp Leu Phe Arg Met Phe Asp Lys Asn Ala Asp Gly Tyr Ile		
100	105	110

Asp Leu Asp Glu Leu Lys Ile Met Leu Gln Ala Thr Gly Glu Thr Ile		
115	120	125

Thr Glu Asp Asp Ile Glu Glu Leu Met Lys Asp Gly Asp Lys Asn Asn		
130	135	140

Asp	Gly	Arg	Ile	Asp	Tyr	Asp	Glu	Phe	Leu	Glu	Phe	Met	Lys	Gly	Val
145						150				155					160

Glu

<210> 21
<211> 633
<212> DNA
<213> Homo sapiens

<400> 21	60
atggcggatg ggagcagcga tgcggctagg gAACCTCGCC ctgcaccAGC cccaatcaga	
cGCCGCTCCT ccaactaccg cgcttatGCC acggagCCGC acGCCAAGAA aaaatctaag	120
atctccgcct cgagaaaatt gcagctgaag actctgctgc tgcagattgc aaagcaagag	180
ctggagcgag aggCGGAGGA GCGGCGCGGA gagaAGGGGC GCGCTCTGAG cacCCGCTGC	240
cAGCCGCTGG agttgaccGG gctgggcttc gcggagctgc aggacttGtg ccgacAGCTC	300
cACGCCCGTG tggacaaggt ggatgaagag agatacGACA tagaggcaa agtcaccaag	360
aacatcacgg agattgcaga tctgactcag aagatcttg accttcgagg caagttaag	420
cggcccacCC tgcggagagt gaggatctc gcagatGCCA tGATGCAGGC gctgctgggg	480
gcccgggcta aggagtccct ggacctgcgg GCCCACCTCA agcaggtgaa gaaggaggac	540
accgagaagg aaaaccggga ggtgggagac tggcggaaaga acatcgatgc actgagtgga	600
atggagggcc gcaagaaaaa gttttagagc tga	633

<210> 22
<211> 210
<212> PRT
<213> Homo sapiens

<400> 22	
Met Ala Asp Gly Ser Ser Asp Ala Ala Arg Glu Pro Arg Pro Ala Pro	
1 5 10 15	

Ala Pro Ile Arg Arg Ser Ser Asn Tyr Arg Ala Tyr Ala Thr Glu	
20 25 30	

Pro His Ala Lys Lys Ser Lys Ile Ser Ala Ser Arg Lys Leu Gln	
35 40 45	

Leu Lys Thr Leu Leu Gln Ile Ala Lys Gln Glu Leu Glu Arg Glu	
50 55 60	

Ala Glu Glu Arg Arg Gly Glu Lys Gly Arg Ala Leu Ser Thr Arg Cys
 65 70 75 80

Gln Pro Leu Glu Leu Thr Gly Leu Gly Phe Ala Glu Leu Gln Asp Leu
 85 90 95

Cys Arg Gln Leu His Ala Arg Val Asp Lys Val Asp Glu Glu Arg Tyr
 100 105 110

Asp Ile Glu Ala Lys Val Thr Lys Asn Ile Thr Glu Ile Ala Asp Leu
 115 120 125

Thr Gln Lys Ile Phe Asp Leu Arg Gly Lys Phe Lys Arg Pro Thr Leu
 130 135 140

Arg Arg Val Arg Ile Ser Ala Asp Ala Met Met Gln Ala Leu Leu Gly
 145 150 155 160

Ala Arg Ala Lys Glu Ser Leu Asp Leu Arg Ala His Leu Lys Gln Val
 165 170 175

Lys Lys Glu Asp Thr Glu Lys Glu Asn Arg Glu Val Gly Asp Trp Arg
 180 185 190

Lys Asn Ile Asp Ala Leu Ser Gly Met Glu Gly Arg Lys Lys Lys Phe
 195 200 205

Glu Ser
 210

<210> 23

<211> 483

<212> DNA

<213> Homo sapiens

<400> 23

atgacggacc agcaggctga ggccaggtcc tacctcagcg aagagatgat cgctgagttc 60

aaggctgcct ttgacatgtt tcatgtgtat ggtgggtgggg acatcagcgt caaggagttg 120

ggcacggta tgaggatgct gggccagaca cccaccaagg aggagctgga cgccatcatc 180

gaggaggtgg atgaggacgg cagcggcacc atcgacttcg aggagttctt ggtcatgtat 240

tgcgccaga tgaaagagga cgcgaaaggg aagagcgagg aggagctggc cgagtgcattc 300

cgcacatcttcg acaggaatgc agacggctac atcgaccggg aggagctggc tgagatttc	360
agggcctccg gggagcacgt gactgacgag gagatcgaat ctctgatgaa agacggcgac	420
aagaacaacg acggccgcat tgacttcgac gagttcctga agatgatgga gggcgtgcag	480
taa	483

<210> 24
<211> 160
<212> PRT
<213> Homo sapiens

<400> 24			
Met Thr Asp Gln Gln Ala Glu Ala Arg Ser Tyr Leu Ser Glu Glu Met			
1	5	10	15

Ile Ala Glu Phe Lys Ala Ala Phe Asp Met Phe Asp Ala Asp Gly Gly		
20	25	30

Gly Asp Ile Ser Val Lys Glu Leu Gly Thr Val Met Arg Met Leu Gly		
35	40	45

Gln Thr Pro Thr Lys Glu Glu Leu Asp Ala Ile Ile Glu Glu Val Asp		
50	55	60

Glu Asp Gly Ser Gly Thr Ile Asp Phe Glu Glu Phe Leu Val Met Met			
65	70	75	80

Val Arg Gln Met Lys Glu Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu		
85	90	95

Ala Glu Cys Phe Arg Ile Phe Asp Arg Asn Ala Asp Gly Tyr Ile Asp		
100	105	110

Pro Glu Glu Leu Ala Glu Ile Phe Arg Ala Ser Gly Glu His Val Thr		
115	120	125

Asp Glu Glu Ile Glu Ser Leu Met Lys Asp Gly Asp Lys Asn Asn Asp		
130	135	140

Gly Arg Ile Asp Phe Asp Glu Phe Leu Lys Met Met Glu Gly Val Gln			
145	150	155	160

<210> 25
<211> 492
<212> DNA
<213> Gallus gallus

<400> 25
atggcgtcaa tgacggacca gcaggcgag gcccgcgcct tcctcagcga ggagatgatt 60
gctgagttca aagctgcctt tgacatgttt gatgcggacg gtggtgaaaa catcagcacc 120
aaggagttgg gcacggtgat gaggatgtg ggcagaacc ccaccaaaga ggagctggat 180
gccatcatcg aggaggtgga cgaggatggc agcggcacca tcgacttcga ggagttcctg 240
gtgatgatgg tgcgcagat gaaagaggac gccaaggggca agtctgagga ggagctggcc 300
aactgcttcc gcatcttcga caagaacgct gatgggttca tcgacatcga ggagctgggt 360
gagattctca gggccactgg ggagcacgatc atcgaggagg acatagaaga cctcatgaag 420
gattcagaca agaacaatga cggccgcatt gacttcgatg agttcctgaa gatgatggag 480
ggtgtgcagt aa 492

<210> 26
<211> 163
<212> PRT
<213> Gallus gallus

<400> 26
Met Ala Ser Met Thr Asp Gln Gln Ala Glu Ala Arg Ala Phe Leu Ser
1 5 10 15

Glu Glu Met Ile Ala Glu Phe Lys Ala Ala Phe Asp Met Phe Asp Ala
20 25 30

Asp Gly Gly Gly Asp Ile Ser Thr Lys Glu Leu Gly Thr Val Met Arg
35 40 45

Met Leu Gly Gln Asn Pro Thr Lys Glu Glu Leu Asp Ala Ile Ile Glu
50 55 60

Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp Phe Glu Glu Phe Leu
65 70 75 80

Val Met Met Val Arg Gln Met Lys Glu Asp Ala Lys Gly Lys Ser Glu
85 90 95

Glu Glu Leu Ala Asn Cys Phe Arg Ile Phe Asp Lys Asn Ala Asp Gly
100 105 110

Phe Ile Asp Ile Glu Glu Leu Gly Glu Ile Leu Arg Ala Thr Gly Glu
 115 120 125

His Val Ile Glu Glu Asp Ile Glu Asp Leu Met Lys Asp Ser Asp Lys
 130 135 140

Asn Asn Asp Gly Arg Ile Asp Phe Asp Glu Phe Leu Lys Met Met Glu
 145 150 155 160

Gly Val Gln

<210> 27
<211> 552
<212> DNA
<213> Gallus gallus

<400> 27
atgtctgatg aagagaaaaa gaggaggca gccaccgccc ggcgccagca cctgaagagt 60
gctatgctcc agcttgctgt cactgaaata gaaaaagaag cagctgctaa agaagtggaa 120
aagcaaaact acctggcaga gcattgcct cctctgtccc tcccaggatc catgcagggaa 180
cttcaggaac tgtgcaaaaaa gcttcatgcc aagatagact cagtgatga ggaaaggtat 240
gacacagagg tgaagctaca gaagactaac aaggagctgg aggacctgag ccagaagctg 300
tttgacctga gggcaagtt caagaggca cctctgcgcc gggtgcgcat gtctgctgat 360
gccatgctgc gtgcctgct gggctccaag cacaaggta acatggacct ccgggccaac 420
ctgaagcaag tcaagaagga ggacacggag aaggagaagg acctccgcga tgtgggtgac 480
tggaggaaga acattgagga gaaatctggc atggagggca ggaagaagat gtttggggcc 540
ggcgagtcct aa 552

<210> 28
<211> 183
<212> PRT
<213> Gallus gallus

<400> 28
Met Ser Asp Glu Glu Lys Lys Arg Arg Ala Ala Thr Ala Arg Arg Gln
1 5 10 15

His Leu Lys Ser Ala Met Leu Gln Leu Ala Val Thr Glu Ile Glu Lys
20 25 30

Glu Ala Ala Ala Lys Glu Val Glu Lys Gln Asn Tyr Leu Ala Glu His
 35 40 45

Cys Pro Pro Leu Ser Leu Pro Gly Ser Met Gln Glu Leu Gln Glu Leu
 50 55 60

Cys Lys Lys Leu His Ala Lys Ile Asp Ser Val Asp Glu Glu Arg Tyr
 65 70 75 80

Asp Thr Glu Val Lys Leu Gln Lys Thr Asn Lys Glu Leu Glu Asp Leu
 85 90 95

Ser Gln Lys Leu Phe Asp Leu Arg Gly Lys Phe Lys Arg Pro Pro Leu
 100 105 110

Arg Arg Val Arg Met Ser Ala Asp Ala Met Leu Arg Ala Leu Leu Gly
 115 120 125

Ser Lys His Lys Val Asn Met Asp Leu Arg Ala Asn Leu Lys Gln Val
 130 135 140

Lys Lys Glu Asp Thr Glu Lys Glu Lys Asp Leu Arg Asp Val Gly Asp
 145 150 155 160

Trp Arg Lys Asn Ile Glu Glu Lys Ser Gly Met Glu Gly Arg Lys Lys
 165 170 175

Met Phe Glu Ala Gly Glu Ser
 180

<210> 29
<211> 486
<212> DNA
<213> Gallus gallus

<400> 29		
atggatgaca tctataaggc ggcgggtttag cagttgacag aagaacaaaa aaatgagtt	60	
aaggctgcct tcgacatctt cgtgctgggg gcagaggatg gctgcattcg caccaaggag	120	
ctggggaaagg tgatgaggat gctggggcag aaccccaccc ctgaggagct gcaggagatg	180	
attgatgagg tggatgagga tggcagtggc actgtggact ttgatgagtt ccttgatatg	240	
atggttcggt gtatgaaaga tgacagcaaa ggaaaaactg aagaggagct ctcagatctc	300	
ttcaggatgt ttgatgaa tgctgatggc tacatcgatc ttgaggaact gaagatcatg	360	

ctacaggcaa ctggagagac gatcaactgag gatgacatag aagaactgat gaaagatggg	420
gacaaaaaca atgatggcag gattgactat gacgagttcc tggagttcat gaagggagtt	480
gaataa	486

<210> 30
<211> 161
<212> PRT
<213> Gallus gallus

<400> 30	
Met Asp Asp Ile Tyr Lys Ala Ala Val Glu Gln Leu Thr Glu Glu Gln	
1	5
	10
	15

Lys Asn Glu Phe Lys Ala Ala Phe Asp Ile Phe Val Leu Gly Ala Glu	
20	25
	30

Asp Gly Cys Ile Ser Thr Lys Glu Leu Gly Lys Val Met Arg Met Leu	
35	40
	45

Gly Gln Asn Pro Thr Pro Glu Glu Leu Gln Glu Met Ile Asp Glu Val	
50	55
	60

Asp Glu Asp Gly Ser Gly Thr Val Asp Phe Asp Glu Phe Leu Val Met	
65	70
	75
	80

Met Val Arg Cys Met Lys Asp Asp Ser Lys Gly Lys Thr Glu Glu	
85	90
	95

Leu Ser Asp Leu Phe Arg Met Phe Asp Lys Asn Ala Asp Gly Tyr Ile	
100	105
	110

Asp Leu Glu Glu Leu Lys Ile Met Leu Gln Ala Thr Gly Glu Thr Ile	
115	120
	125

Thr Glu Asp Asp Ile Glu Glu Leu Met Lys Asp Gly Asp Lys Asn Asn	
130	135
	140

Asp Gly Arg Ile Asp Tyr Asp Glu Phe Leu Glu Phe Met Lys Gly Val	
145	150
	155
	160

Glu

<210> 31
<211> 1878
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 31	
atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggc	60
ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgaggcgaa tgccacctac	120
ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggccccacc	180
ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccgaa ccacatgaag	240
cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc	300
ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg	360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac	420
aagctggagt acaactacat cagccacaac gtctatatca ccgcccacaa gcagaagaac	480
ggcatcaagg cccacttcaa gatccgccccac aacatcgagg acggcagcgt gcagctcgcc	540
gaccactacc agcagaacac ccccatcgcc gacggcccccg tgctgctgcc cgacaaccac	600
tacctgagca cccagtccgc cctgagcaaa gaccccaacg agaagcgcga tcacatggc	660
ctgctggagt tcgtgaccgc cgcccgcatg ctgagcgatg aattgactaa ggagcaaact	720
gcattactac gtaatgcatt taatgcttt gaccctgaaa aaaatggata tatcaacaca	780
gctatgggg gtacgatact tagcatgtt ggtcatcaac ttgatgatgc aactcttgc	840
gacattatcg ctgaagtcga tgaggatggc tcggggccaaa tcgaatttga agaatttacc	900
accctggcag cccgcttcct tgtggaaagag gacgctgaag ctatgatggc tgaattgaag	960
gaagctttcc gccttacga caaagaagga aatggatata taactactgg tggcttcgt	1020
gaaatcctgc gcgaactaga cgataaattt acaaatgacg acctggacat gatgatttag	1080
gaaattgatt ccgatggatc gggtaactgtt gattttgcg aatttatggaa agtaatgacc	1140
ggtgtggcagc acgagctcat ggtgagcaag ggcgaggagc tggccaccgg ggtggcgccc	1200
atcctggtcg agctggacgg cgacgttaaac ggccacaagt tcagcgtgtc cggcgaggcg	1260
gagggcgatg ccacctacgg caagctgacc ctgaagttca tctgcaccac cggcaagctg	1320
cccgccct ggccacccct cgtgaccacc ttccggctacg gcctgatgtg cttcgccccgc	1380
taccccgacc acatgcgcca gcacgacttc ttcaagtccg ccatgccccga aggctacgtc	1440

caggagcgca ccatcttctt caaggacgac ggcaactaca agaccgcgc cgaggtgaag 1500
 ttcgagggcg acaccctggc gagctgaagg gcatcgactt caaggaggac 1560
 ggcacatcc tggggcacaa gctggagttac aactacaaca gccacaaacgt ctatatcatg 1620
 gccgacaaggc agaagaacgg catcaaggcc aacttcaaga tccgccccaa catcgaggac 1680
 ggcagcgtgc agctcgccga ccactaccag cagaacacccc ccatcggcga cggccccgtg 1740
 ctgctgcccc acaaccacta cctgagctac cagtccgccc tgagcaaaga ccccaacgag 1800
 aagcgcgatc acatggtcct gctggagttc gtgaccgccc ccgggatcac tctcggcatg 1860
 gacgagctgt acaagtaa 1878

<210> 32

<211> 625

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 32

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10				15		

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Arg	Phe	Ser	Val	Ser	Gly
			20				25					30			

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
				35		40					45				

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
				50		55			60						

Leu	Thr	Trp	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
				65		70		75				80			

Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
				85				90				95			

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
				100			105				110				

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
				115			120			125					

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Arg Met Leu Ser Asp Glu Leu Thr Lys Glu Gln Thr
225 230 235 240

Ala Leu Leu Arg Asn Ala Phe Asn Ala Phe Asp Pro Glu Lys Asn Gly
245 250 255

Tyr Ile Asn Thr Ala Met Val Gly Thr Ile Leu Ser Met Leu Gly His
260 265 270

Gln Leu Asp Asp Ala Thr Leu Ala Asp Ile Ile Ala Glu Val Asp Glu
275 280 285

Asp Gly Ser Gly Gln Ile Glu Phe Glu Glu Phe Thr Thr Leu Ala Ala
290 295 300

Arg Phe Leu Val Glu Glu Asp Ala Glu Ala Met Met Ala Glu Leu Lys
305 310 315 320

Glu Ala Phe Arg Leu Tyr Asp Lys Glu Gly Asn Gly Tyr Ile Thr Thr
325 330 335

Gly Val Leu Arg Glu Ile Leu Arg Glu Leu Asp Asp Lys Leu Thr Asn
340 345 350

Asp Asp Leu Asp Met Met Ile Glu Glu Ile Asp Ser Asp Gly Ser Gly
 355 360 365

Thr Val Asp Phe Asp Glu Phe Met Glu Val Met Thr Gly Gly Asp Asp
 370 375 380

Glu Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
 385 390 395 400

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
 405 410 415

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
 420 425 430

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
 435 440 445

Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His
 450 455 460

Met Arg Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
 465 470 475 480

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
 485 490 495

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
 500 505 510

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
 515 520 525

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 530 535 540

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 545 550 555 560

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 565 570 575

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
 580 585 590

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 595 600 605

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 610 615 620

Lys
 625

<210> 33
<211> 1866
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 33		
atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac	60	
ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgaggcgaa tgccacctac	120	
ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc	180	
ctcgtgacca ccctgacactg gggcgtgcag tgcttcagcc gctaccccgaa ccacatgaag	240	
cagcacgact tcttcaagtc cgcattcccc gaaggctacg tccaggagcg taccatttc	300	
ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg	360	
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac	420	
aagctggagt acaactacat cagccacaac gtctatatca cccgcgacaa gcagaagaac	480	
ggcatcaagg cccacttcaa gatccgcccc aacatcgagg acggcagcgt gcagctcgcc	540	
gaccactacc agcagaacac ccccatcgcc gacggccccg tgctgctgcc cgacaaccac	600	
tacctgagca cccagtcgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc	660	
ctgctggagt tcgtgaccgc cccccgcattt ctgactaagg agcaaactgc attactacgt	720	
aatgcattta atgctttga ccctgaaaaa aatggatata tcaacacacgc tatggtgggt	780	
acgatactta gcatgttggg tcatcaactt gatgatgcaa ctcttgctga cattatcgct	840	
gaagtcgatg aggatggttc gggccaaatc gaatttgaag aatttaccac cctggcagcc	900	
cgcttccttg tggaagagga cgctgaagct atgatggctg aattgaagga agctttccgc	960	
ctttacgaca aagaaggaaa tggatataata actactggtg ttcttcgtga aatcctgcgc	1020	

gaactagacg ataaattgac aaatgacgac ctggacatga tgattgagga aattgattcc	1080
gatggatcg gtactgttga ttttgatgaa ttatgaaag taatgaccgg tggcgacgac	1140
gagctcatgg tgagcaaggg cgaggagctg ttcaccgggg tggtgcccat cctggtcgag	1200
ctggacggcg acgtaaaacgg ccacaagtgc agcgtgtccg gcgaggcgaa gggcgatgcc	1260
acctacggca agctgaccct gaagttcatc tgaccacccg gcaagctgcc cgtccccctgg	1320
cccaccctcg tgaccaccc ttggctacggc ctgatgtgct tcgcccccta ccccgaccac	1380
atgcgccagc acgacttctt caagtccgcc atgcccgaag gctacgtcca ggagcgacc	1440
atcttttca aggacgacgg caactacaag acccgcccg aggtgaagtt cgagggcgac	1500
accctggtga accgcatcga gctgaaggc atcgacttca aggaggacgg caacatcctg	1560
gggcacaaggc tggagtacaa ctacaacaggc cacaacgtct atatcatggc cgacaaggcag	1620
aagaacggca tcaaggccaa cttcaagatc cgccacaaca tcgaggacgg cagcgtgcag	1680
ctcgccgacc actaccaggc gaacaccccc atcggcgacg gccccgtgct gctgcccgc	1740
aaccactacc ttagctacca gtccggccctg agcaaagacc ccaacgagaa ggcgcgtcac	1800
atggtcctgc tggagttcgt gaccggccgccc gggatcactc tcggcatgga cgagctgtac	1860
aagtaa	1866

<210> 34

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 34

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly		
20	25	30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
35	40	45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
50	55	60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Arg Met Leu Thr Lys Glu Gln Thr Ala Leu Leu Arg
 225 230 235 240

Asn Ala Phe Asn Ala Phe Asp Pro Glu Lys Asn Gly Tyr Ile Asn Thr
 245 250 255

Ala Met Val Gly Thr Ile Leu Ser Met Leu Gly His Gln Leu Asp Asp
 260 265 270

Ala Thr Leu Ala Asp Ile Ile Ala Glu Val Asp Glu Asp Gly Ser Gly
 275 280 285

Gln Ile Glu Phe Glu Glu Phe Thr Thr Leu Ala Ala Arg Phe Leu Val
 290 295 300

Glu Glu Asp Ala Glu Ala Met Met Ala Glu Leu Lys Glu Ala Phe Arg
305 310 315 320

Leu Tyr Asp Lys Glu Gly Asn Gly Tyr Ile Thr Thr Gly Val Leu Arg
325 330 335

Glu Ile Leu Arg Glu Leu Asp Asp Lys Leu Thr Asn Asp Asp Leu Asp
340 345 350

Met Met Ile Glu Glu Ile Asp Ser Asp Gly Ser Gly Thr Val Asp Phe
355 360 365

Asp Glu Phe Met Glu Val Met Thr Gly Gly Asp Asp Glu Leu Met Val
370 375 380

Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
385 390 395 400

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
405 410 415

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
420 425 430

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly
435 440 445

Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His
450 455 460

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
465 470 475 480

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
485 490 495

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
500 505 510

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
515 520 525

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
 530 535 540

Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
 545 550 555 560

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
 565 570 575

Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys
 580 585 590

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
 595 600 605

Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 610 615 620

<210> 35

<211> 465

<212> DNA

<213> Drosophila melanogaster

<400> 35
 atgagcgtatg aattgactaa ggagcaaact gcattactac gtaatgcatt taatgcttt 60
 gaccctgaaa aaaatggata tatcaacaca gctatggtgg gtacgatact tagcatgttg 120
 ggtcatcaac ttgatgatgc aactcttgct gacattatcg ctgaagtcga tgaggatgg 180
 tcggggccaaa tcgaatttga agaatttacc accctggcag cccgcttcct tgtggaagag 240
 gacgctgaag ctatgatggc tgaattgaag gaagcttcc gccttacga caaagaagga 300
 aatggatata taactactgg tttcttcgt gaaatcctgc gcgaactaga cgataaattg 360
 acaaatgacg acctggacat gatgattgag gaaattgatt ccgatggatc gggtaacttt 420
 gattttgatg aatttatgga agtaatgacc ggtggcgacg actaa 465

<210> 36

<211> 154

<212> PRT

<213> Drosophila melanogaster

<400> 36
 Met Ser Asp Glu Leu Thr Lys Glu Gln Thr Ala Leu Leu Arg Asn Ala
 1 5 10 15

Phe Asn Ala Phe Asp Pro Glu Lys Asn Gly Tyr Ile Asn Thr Ala Met
 20 25 30

Val Gly Thr Ile Leu Ser Met Leu Gly His Gln Leu Asp Asp Ala Thr
 35 40 45

Leu Ala Asp Ile Ile Ala Glu Val Asp Glu Asp Gly Ser Gly Gln Ile
 50 55 60

Glu Phe Glu Glu Phe Thr Thr Leu Ala Ala Arg Phe Leu Val Glu Glu
 65 70 75 80

Asp Ala Glu Ala Met Met Ala Glu Leu Lys Glu Ala Phe Arg Leu Tyr
 85 90 95

Asp Lys Glu Gly Asn Gly Tyr Ile Thr Thr Gly Val Leu Arg Glu Ile
 100 105 110

Leu Arg Glu Leu Asp Asp Lys Leu Thr Asn Asp Asp Leu Asp Met Met
 115 120 125

Ile Glu Glu Ile Asp Ser Asp Gly Ser Gly Thr Val Asp Phe Asp Glu
 130 135 140

Phe Met Glu Val Met Thr Gly Gly Asp Asp
 145 150

<210> 37
<211> 468
<212> DNA
<213> Drosophila melanogaster

<400> 37	
atggacaaca ttgacgaaga cctgaccccc gagcagattt ccgttctgca gaaggcattc	60
aacagcttcg accaccagaa gaccggcagt atccccacccg aaatggtggc cgatatcctc	120
cgtcttatgg gtcagccctt cgacaggcag atccttgacg agctgtatgc cgaggtcgat	180
gaggacaaat ccggtcgcct ggagttcgag gagttcgtcc agctggctgc caagttcatc	240
gttagaggagg atgatgaggc catgcagaag gacgtgcgcg aggcttccg tctgtacgac	300
aagcagggca atggctacat tcccacctcc tgccctgaagg agatcctcaa ggaactggac	360
gaccagctga ccgaacagga gctcgacatc atgattgagg aaatcgattc cgacggctct	420
ggcacccgttg attttgatga attcatggag atgatgactg gcgagtaa	468

<210> 38
<211> 155
<212> PRT
<213> Drosophila melanogaster

<400> 38
Met Asp Asn Ile Asp Glu Asp Leu Thr Pro Glu Gln Ile Ala Val Leu
1 5 10 15

Gln Lys Ala Phe Asn Ser Phe Asp His Gln Lys Thr Gly Ser Ile Pro
20 25 30

Thr Glu Met Val Ala Asp Ile Leu Arg Leu Met Gly Gln Pro Phe Asp
35 40 45

Arg Gln Ile Leu Asp Glu Leu Met His Glu Val Asp Glu Asp Lys Ser
50 55 60

Gly Arg Leu Glu Phe Glu Glu Phe Val Gln Leu Ala Ala Lys Phe Ile
65 70 75 80

Val Glu Glu Asp Asp Glu Ala Met Gln Lys Asp Val Arg Glu Ala Phe
85 90 95

Arg Leu Tyr Asp Lys Gln Gly Asn Gly Tyr Ile Pro Thr Ser Cys Leu
100 105 110

Lys Glu Ile Leu Lys Glu Leu Asp Asp Gln Leu Thr Glu Gln Glu Leu
115 120 125

Asp Ile Met Ile Glu Glu Ile Asp Ser Asp Gly Ser Gly Thr Val Asp
130 135 140

Phe Asp Glu Phe Met Glu Met Met Thr Gly Glu
145 150 155

<210> 39
<211> 468
<212> DNA
<213> Drosophila melanogaster

<400> 39
atgagcagcg tcgatgaaga tcttacaccc gagcagatcg ccgtgctcca gaaggcgttc 60
aacagcttcg atcaccagaa gactggctcc atccccaccc agatggtcgc cgacatcctg 120
cgccctgatgg gtcagccctt cgacaagaag atcctggagg aactgatcga ggaggtcgt 180

gaggacaagt ccggtcgctt ggaattcggc gagttcggtcc agctggctgc caagttcatc	240
gtggaggagg atgcggaggc catgcagaag gagctggccg aggcggtccg tttgtacgt	300
aagcagggca atggcttcat tcccaccacc tgccctgaagg agatcctcaa ggagctggac	360
gaccagctga ccgaacagga gctggacatt atgatcgagg agatcgattc cgatggctcc	420
ggtacagtgg atttcgatga attcatggag atgatgactg gcgagtaa	468

<210> 40

<211> 155

<212> PRT

<213> Drosophila melanogaster

<400> 40

Met Ser Ser Val Asp Glu Asp Leu Thr Pro Glu Gln Ile Ala Val Leu			
1	5	10	15

Gln Lys Ala Phe Asn Ser Phe Asp His Gln Lys Thr Gly Ser Ile Pro		
20	25	30

Thr Glu Met Val Ala Asp Ile Leu Arg Leu Met Gly Gln Pro Phe Asp		
35	40	45

Lys Lys Ile Leu Glu Glu Leu Ile Glu Glu Val Asp Glu Asp Lys Ser		
50	55	60

Gly Arg Leu Glu Phe Gly Glu Phe Val Gln Leu Ala Ala Lys Phe Ile			
65	70	75	80

Val Glu Glu Asp Ala Glu Ala Met Gln Lys Glu Leu Ala Glu Ala Phe		
85	90	95

Arg Leu Tyr Asp Lys Gln Gly Asn Gly Phe Ile Pro Thr Thr Cys Leu		
100	105	110

Lys Glu Ile Leu Lys Glu Leu Asp Asp Gln Leu Thr Glu Gln Glu Leu		
115	120	125

Asp Ile Met Ile Glu Glu Ile Asp Ser Asp Gly Ser Gly Thr Val Asp		
130	135	140

Phe Asp Glu Phe Met Glu Met Met Thr Gly Glu		
145	150	155

<210> 41
<211> 1833
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 41		
atgggccccg ccatgaagat cgagtgcgc atcacggca ccctgaacgg cgtggagttc	60	
gagctggtgg gcggcgaga gggcacccc gagcaggcc gcatgaccaa caagatgaag	120	
agcaccaagg gcgcctgac cttcagcccc tacctgtga gccacgtat gggctacggc	180	
ttctaccact tcggcaccta ccccagcgcc tacgagaacc cttcctgca cgccatcaac	240	
aacggcggct acaccaaacac ccgcacatcgag aagtacgagg acggcggcgt gctgcacgtg	300	
agttcagct accgctacga ggccggccgc gtgatcgccg acttcaaggt ggtgggcacc	360	
ggcttccccg aggacagcgt gatttcacc gacaagatca tccgcagcaa cgccaccgtg	420	
gagcacctgc accccatggg cgataacgtg ctggtggca gttcgcccg cacttcagc	480	
ctgcgcgacg gcggctacta cagttcgat gtggacagcc acatgcactt caagagcgc	540	
atccacccca gcatcctgca gaacggggc cccatgtcg cttccgccc cgtggaggag	600	
ctgcacagca acaccgagct gggcatcgat gaggaccgc acgccttcaa gaccccgatc	660	
gcattcgccc gcatgctcag cgaggagatg attgctgagt tcaaagctgc ctttgacatg	720	
tttgatgcgg acgggtgggg ggacatcagc accaaggagt tggcacgggt gatgaggatg	780	
ctgggccaga accccaccaa agaggagctg gatccatca tcgaggaggt ggacgaggat	840	
ggcagcggca ccatcgactt cgaggagttc ctggatgtga tggcgccca gatgaaagag	900	
gacgccaagg gcaagtctga ggaggagctg gccaactgtc tccgcatttt cgacaagaac	960	
gctgatgggt tcatcgacat cgaggagctg ggtgagattc tcaggccac tggggagcac	1020	
gtcatcgagg aggacataga agacctcatg aaggattcag acaagaacaa tgacggccgc	1080	
attgacttcg atgagttcct gaagatgtatg gaggggtgtgc aggagctcat gtccagcggc	1140	
gccctgctgt tccacggcaa gatcccctac gtgggtggaga tggagggcaa tgtggatggc	1200	
cacaccttca gcatcccgccg caagggtac ggcgtgcac gctggggcaa ggtggatgcc	1260	
cagttcatct gcaccacccgg cgatgtgtcc gtgcctgga gcaccctggt gaccaccctg	1320	
acctacggcg cccagtgctt cgccaagtac ggccccgagc tgaaggattt ctacaagagc	1380	
tgcacatggccg atggctacgt gcaggagcgc accatcacct tcgagggcga tggcaatttc	1440	

aagaccgcg ccgagggtgac cttcgagaat ggcagcgtgt acaatcgcgt gaagctgaat	1500
ggccagggcgt tcaagaagga tggccacgtg ctgggcaaga atctggagtt caatttcacc	1560
ccccactgccc tgtacatctg gggcgatcag gccaatcacg gcctgaagag cgcccttcaag	1620
atctgccacg agatcacccgg cagcaagggc gatttcatcg tggccgatca cacccagatg	1680
aataccccca tcggcggcgg ccccgtgcac gtgcccagt accaccacat gagctaccac	1740
gtgaagctga gcaaggatgt gaccgatcac cgcgataata tgagcctgaa ggagaccgtg	1800
cgccgcgtgg attgccgcaa gacacctctg tga	1833

<210> 42

<211> 610

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 42

Met	Gly	Pro	Ala	Met	Lys	Ile	Glu	Cys	Arg	Ile	Thr	Gly	Thr	Leu	Asn
1				5					10					15	

Gly	Val	Glu	Phe	Glu	Leu	Val	Gly	Gly	Gly	Glu	Gly	Thr	Pro	Glu	Gln
					20			25					30		

Gly	Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Ala	Leu	Thr	Phe
	35					40					45				

Ser	Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly	Tyr	Gly	Phe	Tyr	His	Phe
	50				55				60						

Gly	Thr	Tyr	Pro	Ser	Gly	Tyr	Glu	Asn	Pro	Phe	Leu	His	Ala	Ile	Asn
	65				70			75				80			

Asn	Gly	Gly	Tyr	Thr	Asn	Thr	Arg	Ile	Glu	Lys	Tyr	Glu	Asp	Gly	Gly
	85					90					95				

Val	Leu	His	Val	Ser	Phe	Ser	Tyr	Arg	Tyr	Glu	Ala	Gly	Arg	Val	Ile
		100				105					110				

Gly	Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Glu	Asp	Ser	Val	Ile
	115				120				125						

Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His
 130 135 140

Pro Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser
 145 150 155 160

Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His
 165 170 175

Phe Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met
 180 185 190

Phe Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly
 195 200 205

Ile Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala Arg
 210 215 220

Met Leu Ser Glu Glu Met Ile Ala Glu Phe Lys Ala Ala Phe Asp Met
 225 230 235 240

Phe Asp Ala Asp Gly Gly Asp Ile Ser Thr Lys Glu Leu Gly Thr
 245 250 255

Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys Glu Glu Leu Asp Ala
 260 265 270

Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp Phe Glu
 275 280 285

Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu Asp Ala Lys Gly
 290 295 300

Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg Ile Phe Asp Lys Asn
 305 310 315 320

Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly Glu Ile Leu Arg Ala
 325 330 335

Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu Asp Leu Met Lys Asp
 340 345 350

Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe Asp Glu Phe Leu Lys
 355 360 365

Met Met Glu Gly Val Gln Glu Leu Met Ser Ser Gly Ala Leu Leu Phe
370 375 380

His Gly Lys Ile Pro Tyr Val Val Glu Met Glu Gly Asn Val Asp Gly
385 390 395 400

His Thr Phe Ser Ile Arg Gly Lys Gly Tyr Gly Asp Ala Ser Val Gly
405 410 415

Lys Val Asp Ala Gln Phe Ile Cys Thr Thr Gly Asp Val Pro Val Pro
420 425 430

Trp Ser Thr Leu Val Thr Thr Leu Thr Tyr Gly Ala Gln Cys Phe Ala
435 440 445

Lys Tyr Gly Pro Glu Leu Lys Asp Phe Tyr Lys Ser Cys Met Pro Asp
450 455 460

Gly Tyr Val Gln Glu Arg Thr Ile Thr Phe Glu Gly Asp Gly Asn Phe
465 470 475 480

Lys Thr Arg Ala Glu Val Thr Phe Glu Asn Gly Ser Val Tyr Asn Arg
485 490 495

Val Lys Leu Asn Gly Gln Gly Phe Lys Lys Asp Gly His Val Leu Gly
500 505 510

Lys Asn Leu Glu Phe Asn Phe Thr Pro His Cys Leu Tyr Ile Trp Gly
515 520 525

Asp Gln Ala Asn His Gly Leu Lys Ser Ala Phe Lys Ile Cys His Glu
530 535 540

Ile Thr Gly Ser Lys Gly Asp Phe Ile Val Ala Asp His Thr Gln Met
545 550 555 560

Asn Thr Pro Ile Gly Gly Pro Val His Val Pro Glu Tyr His His
565 570 575

Met Ser Tyr His Val Lys Leu Ser Lys Asp Val Thr Asp His Arg Asp
580 585 590

Asn Met Ser Leu Lys Glu Thr Val Arg Ala Val Asp Cys Arg Lys Thr
595 600 605

Tyr Leu
610

<210> 43
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 43
Gly Gly Ser Gly Gly
1 5

<210> 44
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 44
Met Leu Leu Ser Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala
1 5 10 15

Ala Asp

<210> 45
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 45
Lys Asp Glu Leu
1

<210> 46
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 46

Met Leu Cys Cys Met Arg Arg Thr Lys Gln Val Glu Lys Asn Asp Glu
1 5 10 . 15Asp Gln Lys Ile
20

<210> 47

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 47

Lys Leu Asn Pro Pro Asp Glu Ser Gly Thr Gly Cys Met Ser Cys Lys
1 5 10 . 15Cys Val Leu Ser
20

<210> 48

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 48

Val Tyr Glu Lys Leu Ser Ser Ile Glu Ser Asp Val
1 5 10

<210> 49

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 49

Met Gln Ala Ala Thr Leu Pro Leu Asp Asn Ile Ser Tyr Arg Arg Glu
1 5 10 . 15

Ser Ala Ile

<210> 50
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 50 .
gccccacca tgg

13

<210> 51
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 51
Lys Leu Asn Pro Pro Asp Glu Ser Gly Pro Gly Cys Met Ser Cys Lys
1 5 10 15

Cys Val Leu Ser
20

<210> 52
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 52
Met Gly Cys Cys Met Arg Arg Thr Lys Gln Val Glu Lys Asn Asp Glu
1 5 10 15

Asp Gln Lys Ile
20

<210> 53
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 53
Gly Gly Thr Gly Gly Ser
1 5

<210> 54
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 54
gccggccacca tggcc